

## SEQUENCE LISTING

<110> Lu, Min  
Ji, Hong

<120> Antigen for Developing Neutralizing Antibodies to Human Immunodeficiency Virus

<130> 1676.002US1

<140> 09/877,606

<141> 2001-06-08

<150> US 60/210,322

<151> 2000-06-08

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> The amino acid sequence of the COOH-terminal extension of gp41.

<400> 1

Asn	Glu	Gln	Glu	Leu	Leu	Glu	Leu	Asp	Lys	Trp	Gly	Thr	Lys	Ile	Lys
1				5					10					15	
Gln	Ile	Glu	Asp	Lys	Ile	Glu	Glu	Ile	Leu	Ser	Lys	Ile	Tyr	His	Ile
			20					25					30		
Glu	Asn	Glu	Ile	Ala	Arg	Ile	Lys	Lys	Leu	Ile	Gly	Glu	Arg		
		35					40					45			

<210> 2

<211> 78

<212> PRT

<213> Artificial Sequence

<220>

<223> Linear amino acid sequence of a helical wheel projection of C45-pII.

<400> 2

Asn	His	Thr	Thr	Trp	Leu	Glu	Trp	Asp	Arg	Glu	Ile	Asn	Asn	Tyr	Thr
1				5					10					15	
Ser	Leu	Ile	His	Ser	Leu	Ile	Glu	Glu	Ser	Gln	Asn	Gln	Gln	Glu	Lys
			20					25					30		
Asn	Glu	Gln	Glu	Leu	Leu	Glu	Leu	Asp	Lys	Trp	Ala	Ser	Lys	Ile	Lys
		35					40					45			
Gln	Ile	Glu	Asp	Lys	Ile	Glu	Glu	Ile	Leu	Ser	Lys	Ile	Tyr	His	Ile
	50					55			60						
Glu	Asn	Glu	Ile	Ala	Arg	Ile	Lys	Lys	Leu	Ile	Gly	Glu	Arg		
65					70					75					

<210> 3  
 <211> 52  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Amino acid sequence of C52.

<400> 3  
 Asn His Thr Thr Trp Leu Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr  
 1 5 10 15  
 Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys  
 20 25 30  
 Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn  
 35 40 45  
 Trp Phe Asn Ile  
 50

<210> 4  
 <211> 85  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> The chimera of the C52 peptide and an isoleucine-zipper trimer (GCN4-pII).

<400> 4  
 Asn His Thr Thr Trp Leu Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr  
 1 5 10 15  
 Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys  
 20 25 30  
 Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn  
 35 40 45  
 Trp Phe Asn Ile Lys Ile Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile  
 50 55 60  
 Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys  
 65 70 75 80  
 Leu Ile Gly Glu Arg  
 85

<210> 5  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Most common sequence of amino acids at positions 669-675 of gp160 (M group HIV-1 strain).

<400> 5  
 Leu Trp Asn Trp Phe Asp Ile  
 1 5

<210> 6  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Amino acid sequence immediately NH2-terminal to SEQ ID NO:5.

<400> 6

Glu Leu Asp Lys Trp Ala

1

5

<210> 7

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acids 669-675 of gp41.

<400> 7

Leu Trp Asn Trp Phe Asn Ile

1

5

<210> 8

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acids at positions 669-675 of gp160.

<221> SITE

<222> 1

<223> Xaa = Leu, Ile, Val, or Ser.

<221> SITE

<222> 2

<223> Xaa = tryptophan or no amino acid present due to the presence of a stop codon at this position in the reading frame.

<221> SITE

<222> 3

<223> Xaa = Asn, Ser, Thr, or Asp or no amino acid present due to the presence of a stop codon at an earlier position in the reading frame.

<221> SITE

<222> 4

<223> Xaa = Trp or no amino acid present due to the presence of a stop codon at this position or at an earlier position in the reading frame.

<221> SITE

<222> 5

<223> Xaa = Phe, Leu, Tyr, or Ser or no amino acid present due to the presence of a stop codon at an earlier position in the reading frame.

<221> SITE

<222> (6)...(6)

<223> Xaa = Asp, Ser, Asn, Gly, Thr, Glu, or no amino acid present due to the presence of a stop codon at this position or an earlier position in the reading frame.

<221> SITE

<222> (7)...(7)

<223> Xaa = Ile or Met or no amino acid present due to the presence of a stop codon at an earlier position in the reading frame.

<400> 8

Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1

5

<210> 9

<211> 52

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant (N656L) amino acid sequence of C52.

<400> 9

Asn His Thr Thr Trp Leu Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr  
1 5 10 15

Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys  
20 25 30

Leu Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn  
35 40 45

Trp Phe Asn Ile  
50